

Meiofauna in Antarctic sea ice - pack ice vs. fast ice

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This poster shows preliminary results from an Antarctic expedition with RV Polarstern from Dec 2014-Feb 2015 with the following:

Study Area

Pack-ice stations: 32, 35
Fast-ice stations: 40-1, 40-3, 40-5, 46, 58

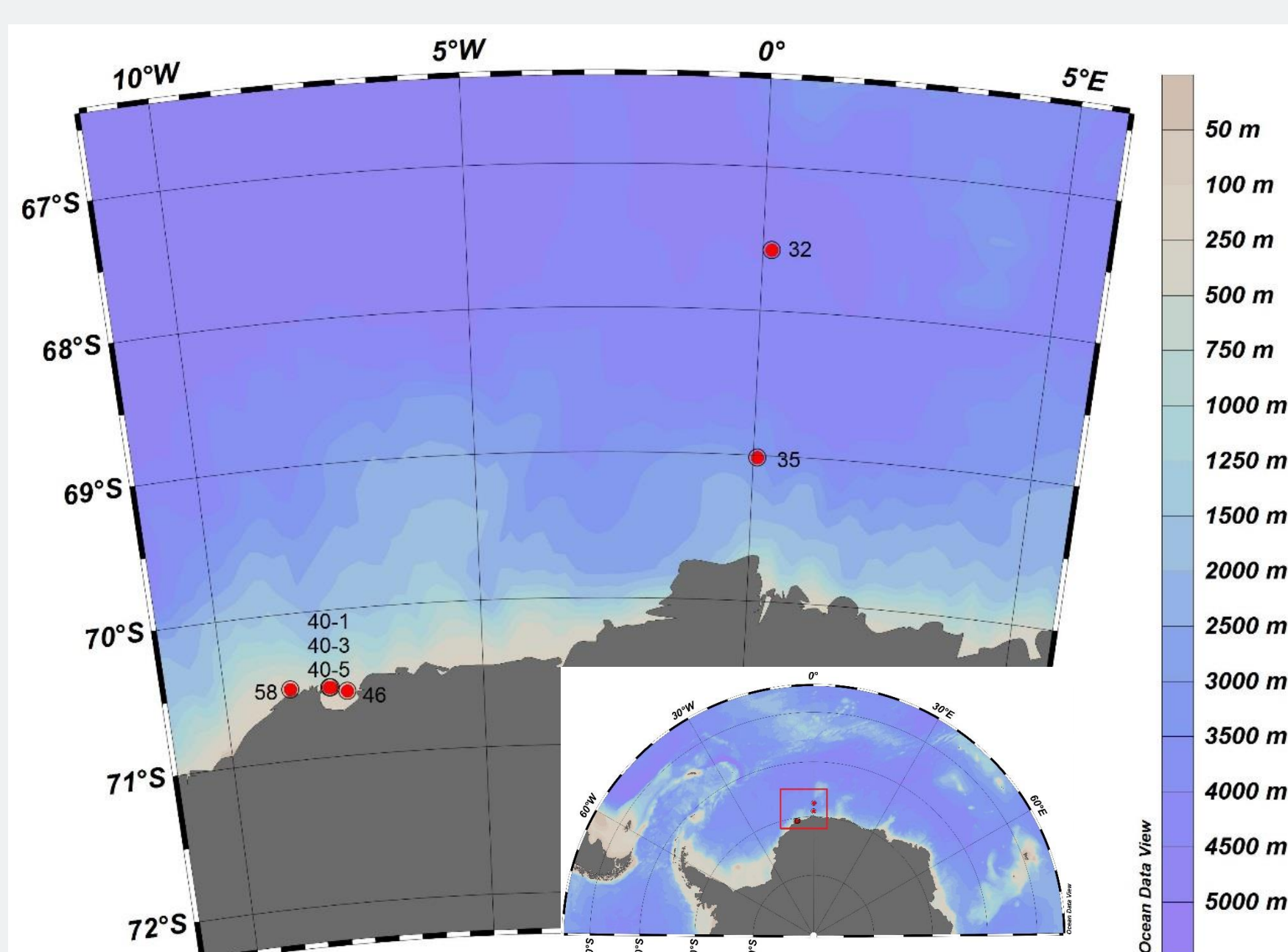


Figure 1 Station plot of 7 ice-stations during the RV Polarstern expedition with pack-ice stations: 32, 35 and fast-ice stations: 40-1, 40-3, 40-5, 46, 58 (Schlitzer, R., Ocean Data View, <http://odv.awi.de>, 2014)

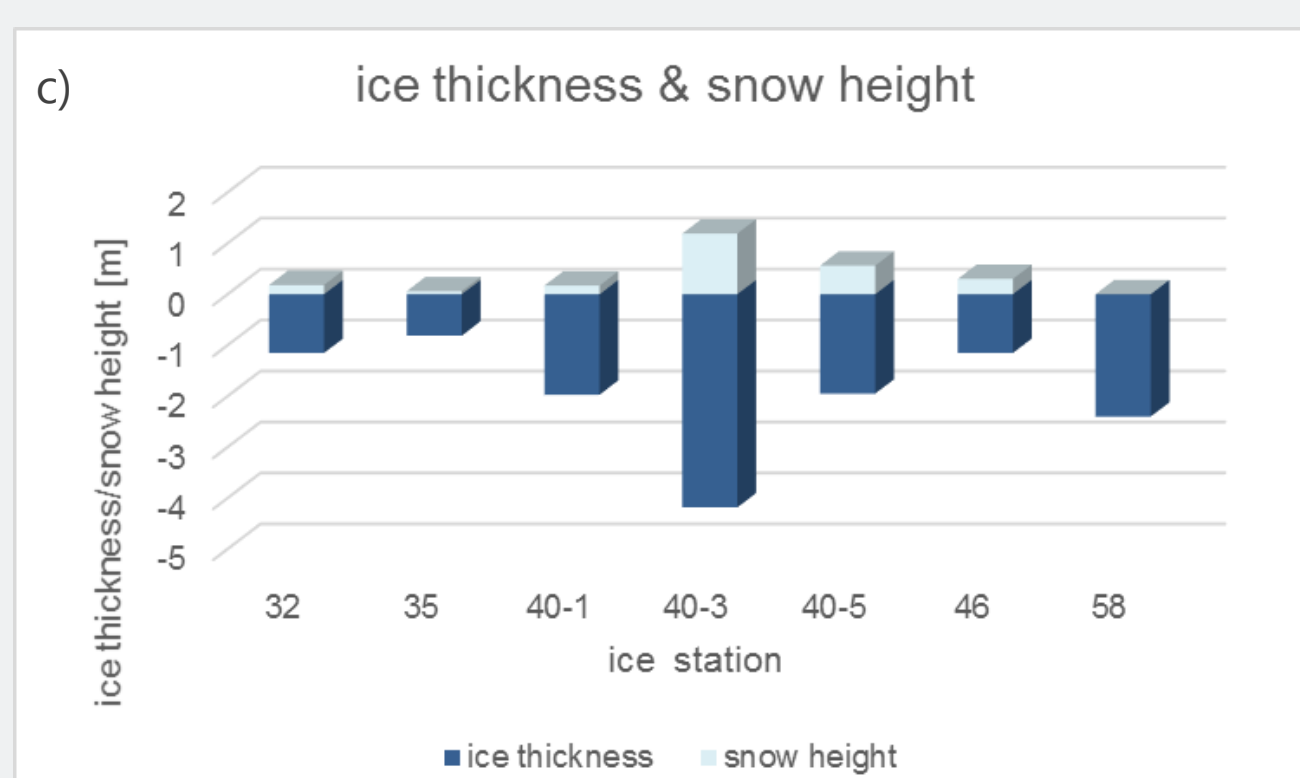
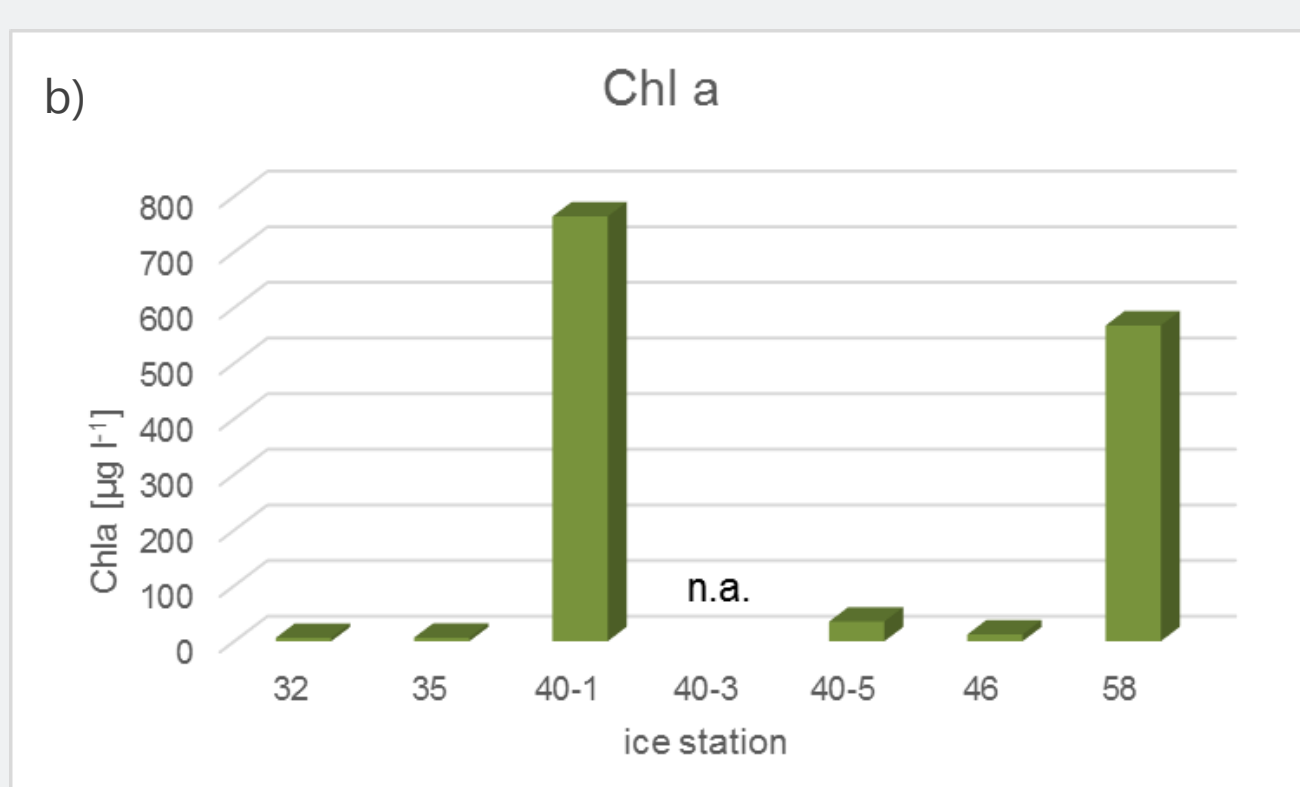
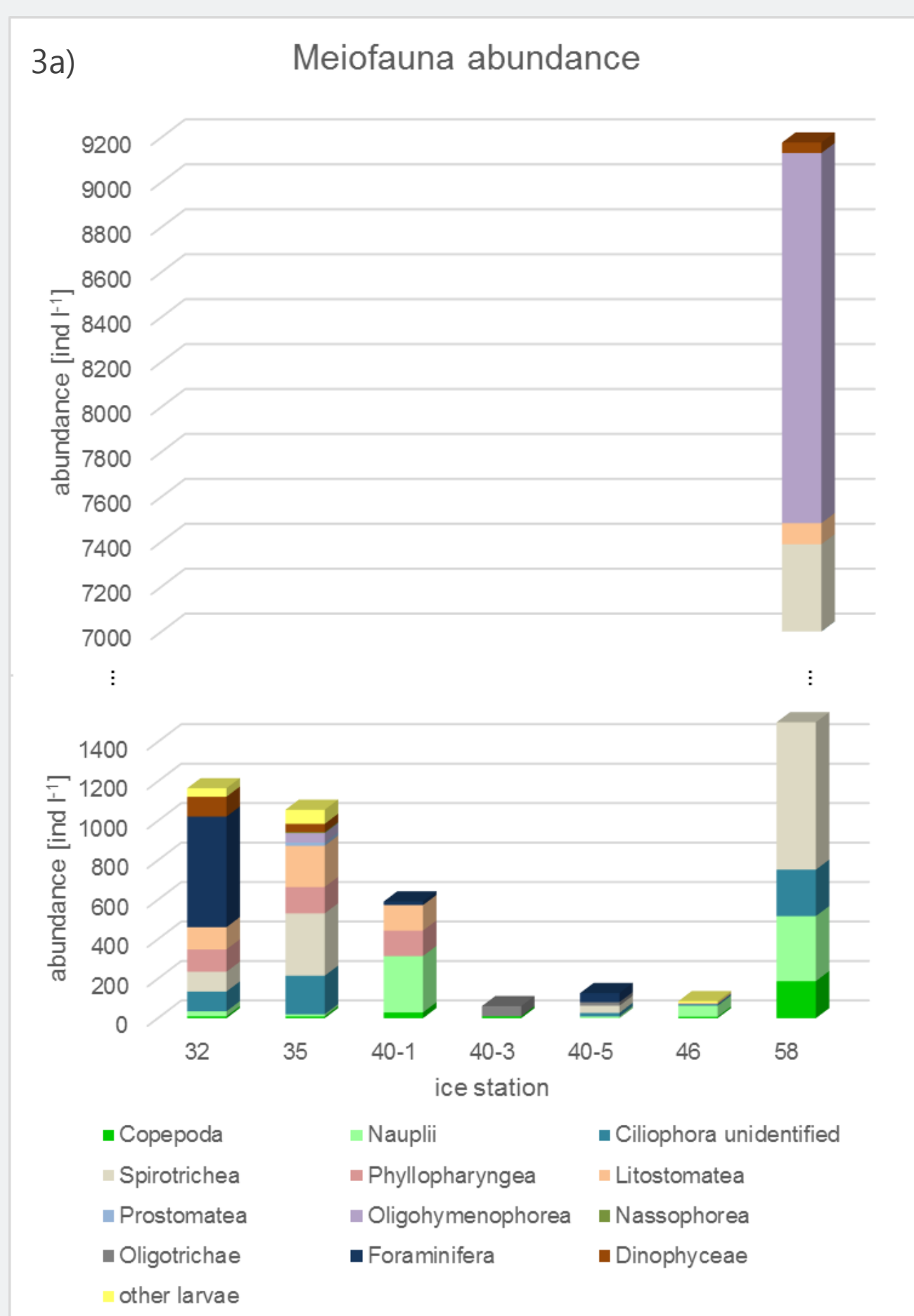


Figure 3a) Meiofauna composition for 7 ice stations: the abundance of main taxa in individuals per liter b) Chlorophyll a concentration for 7 ice stations in µg per liter c) Ice thickness and snow height for 7 ice stations in meter

Objectives

Analysis of the community composition and abundance of sea-ice meiofauna

Comparison of the results with state of the art molecular techniques

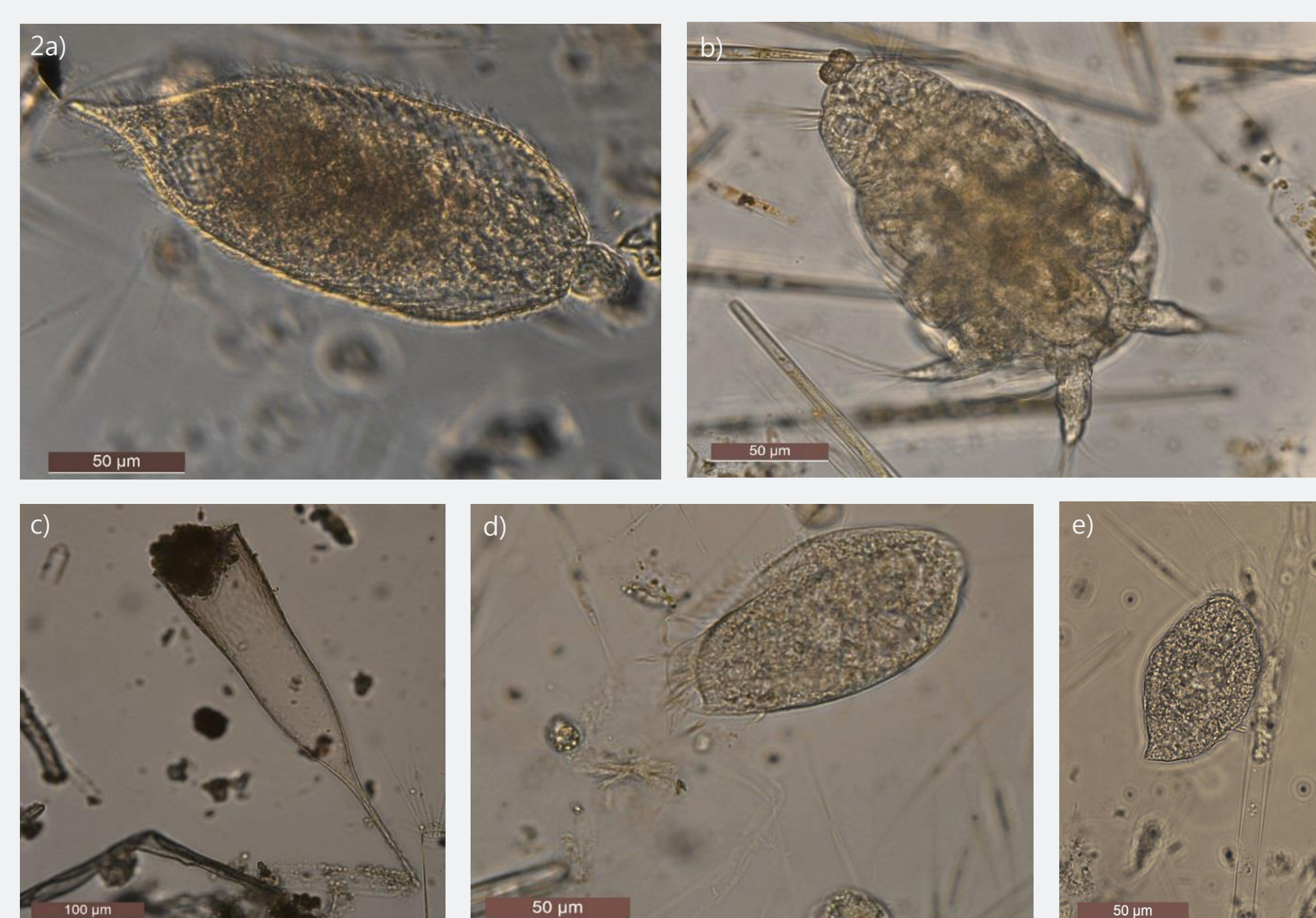


Figure 2 Pictures of a) Litostomatea b) Nauplii c) Oligotrichae d) Spirotrichea and e) Phyllopharyngea

Preliminary results

- With microscopy 23 taxa of Meiofauna could be identified for all 7 ice stations.
- The pack-ice stations are more diverse and abundant than the fast-ice stations, except station 58 which stands out. Within fast-ice stations there is a correlation between the abundance of Meiofauna and Chl a concentration.
- Ciliophora and Foraminifera dominated the pack-ice stations whereas fast-ice stations were dominated by Ciliophora and Copepoda.
- The same classes of Ciliophora were found with microscopic- and molecular analysis. The pack-ice stations were more diverse than the fast-ice stations. The most dominant classes were Spirotrichea and Litostomatea.

Conclusion

The results of the microscopic- as well as of the molecular analysis categorized the meiofauna into two ecotypes which are associated with the ice types (pack ice and fast ice).

Materials and methods

Ice cores from 7 ice stations were taken with a driller (Ø 9cm). The bottom 10cm of every ice core was cut off and analyzed by:

Microscopy

Ice cores were filtered through 10µm mesh. For determining and counting microzooplankton the sample was analyzed with the Utermöhl-method. For determining and counting bigger organisms the whole sample was put in a Bogorov counting chamber for microscopy.

Molecular biology

The samples were filtered through 0.4µm and DNA was isolated. A PCR amplification of target DNA fragments (V4 region of 18S rDNA), library preparation and next-generation sequencing (MiSeq, Illumina) was performed. The sequence data were analyzed using the bioinformatic pipeline QIIME. As a taxonomic reference the SILVA data base was used.

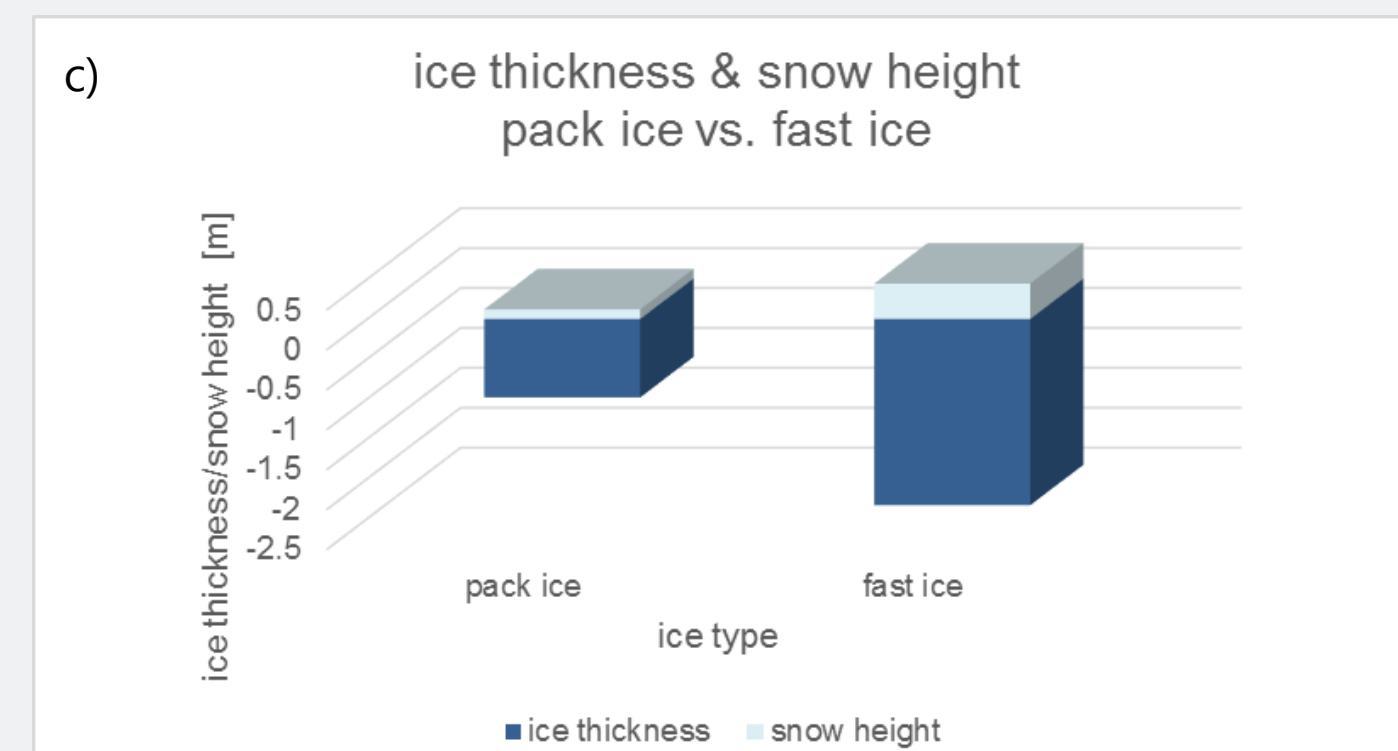
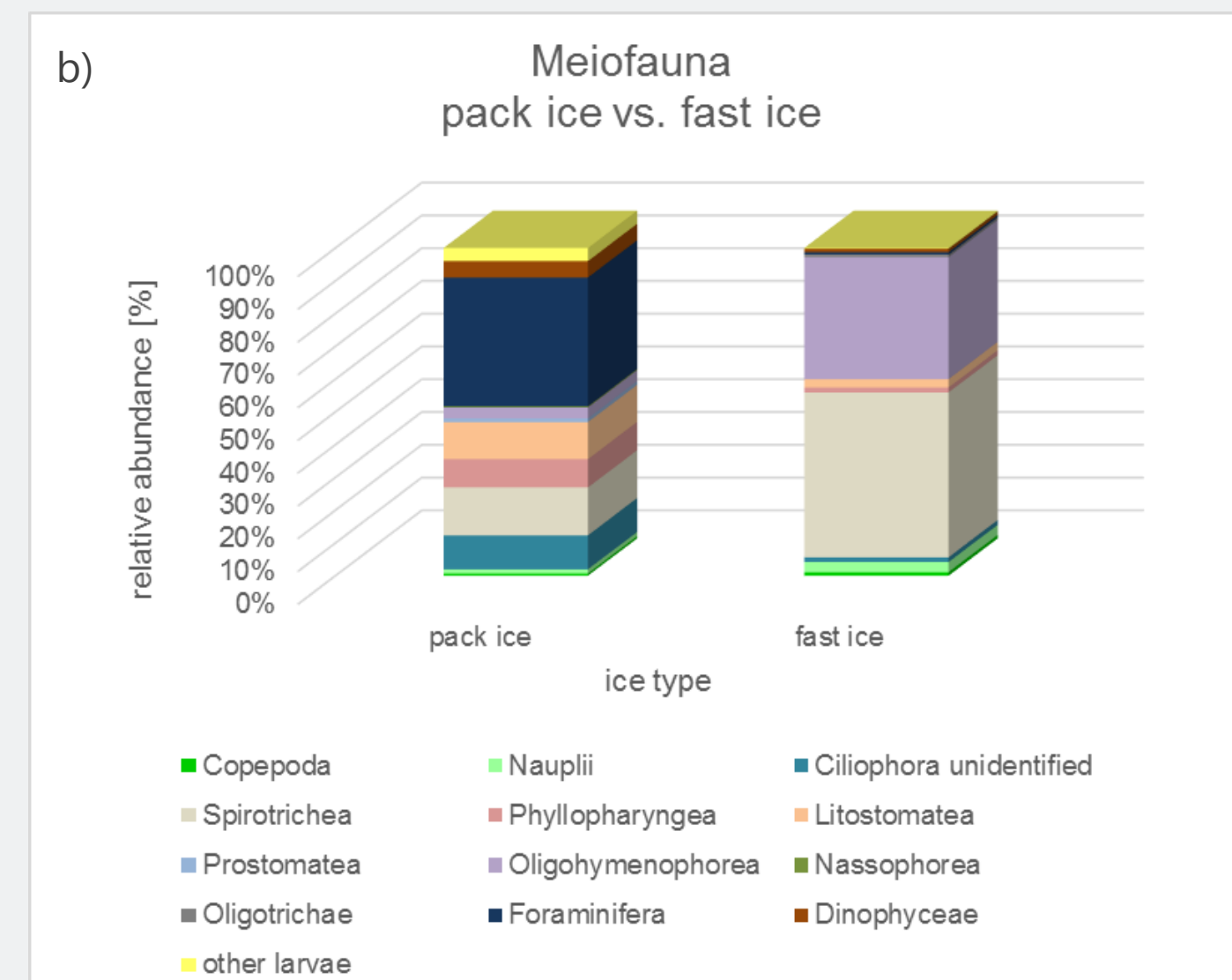
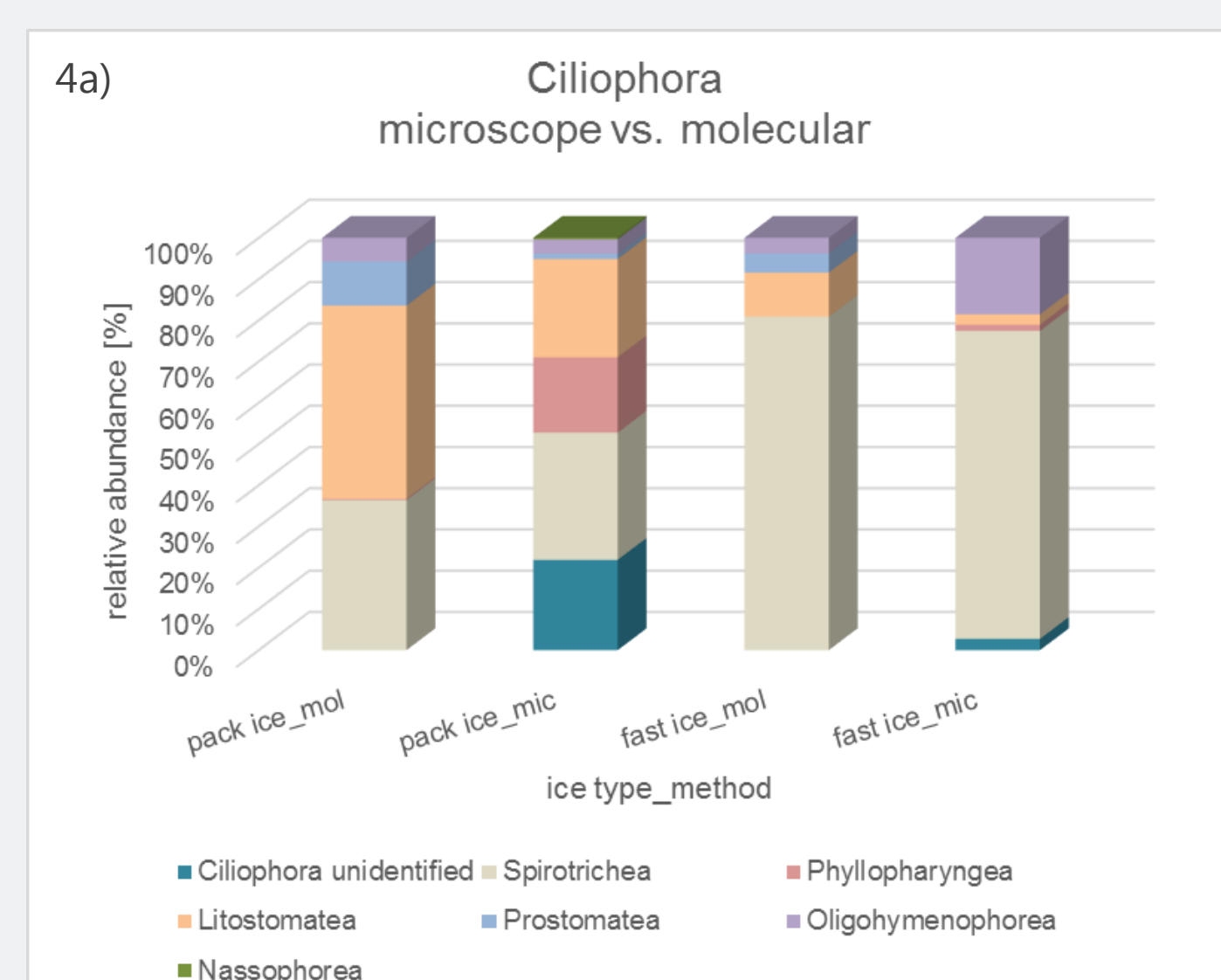


Figure 4a) Ciliophora composition for pack ice and fast ice in % for two different methods of analyzing b) Meiofauna composition for pack ice and fast ice: the main taxa in relative abundance c) Ice thickness and snow height for pack ice and fast ice in meter

